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R. Hutson

1652
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FEB 14 2001

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/462,846 DATE: 02/02/2001
TIME: 16:35:53

Input Set : A:\GC381-US-seqlist.txt
Output Set: N:\CRF3\02022001\I462846.raw

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3 <110> APPLICANT: Estell, David A.
5 <120> TITLE OF INVENTION: Proteases From Gram-Positive Organisms
8 <130> FILE REFERENCE: GC381-US
10 <140> CURRENT APPLICATION NUMBER: US 09/462,846
11 <141> CURRENT FILING DATE: 2000-01-13
13 <150> PRIOR APPLICATION NUMBER: PCT/US98/19529
14 <151> PRIOR FILING DATE: 1998-07-14
16 <150> PRIOR APPLICATION NUMBER: EP 97305227.7
17 <151> PRIOR FILING DATE: 1997-07-15
19 <160> NUMBER OF SEQ ID NOS: 7
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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24 <211> LENGTH: 945
25 <212> TYPE: DNA
26 <213> ORGANISM: Bacillus subtilis
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30 gctttagctg attttggcta taccattccg tcacaacgaa caggggagtg ctgggctttt 120
31 gccgcgcac aaaatggtca aagcgttggt caaaacggaa tgtataaggg gttcacgctc 180
32 agcgaattat ggaacatca cagacattta ttccggacagc ttgaagggga cggtttcctt 240
33 ctgcttacia aaatattaga tgctgaccag gacttatctg ttccgggtga tccgaatgat 300
34 gaatatgcca acatacatga aaacggtgag cttggaaaaa cagaatgctg gtacattatt 360
35 gattgcaaaa aagatgccga gattatttat ggcacaaatg caacaacaaa ggaagaacta 420
36 actaccatga tagagcgtgg agaattggat gagctcttgc gccgtgtaaa ggtaaaagccg 480
37 ggggattttt tctatgtgcc aagcgttact gttcatgcga ttggaaaagg aattcttget 540
38 ttggagagcg agcagaactc agacacaacc tacagattat atgattatga ccgaaaagat 600
39 gcagaaggca agctgcgcga gcttcactct aaaaagagca ttgaagtgat agaggtccc 660
40 tctattccag aacggcatac agttcaccat gaacaaattg aggatttgc tacaacgaca 720
41 ttgattgaat gcgcttactt ttccgtgggg aaatggaaact ttcaggatc agcaagctta 780
42 aagcagcaaaa aaccattcct tcttatcagt gtgattgaag gggagggccg tatgatctct 840
43 ggtgagtatg tctatccttt caaaaaagga gatcatatgt tgcgcctta cggctcttga 900
44 gaatttaaac tcgaaggata tgcagaatgt atcgtctccc atctg 945
46 <210> SEQ ID NO: 2
47 <211> LENGTH: 315
48 <212> TYPE: PRT
49 <213> ORGANISM: Bacillus subtilis
51 <400> SEQUENCE: 2
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55 20 25 30
56 Arg Thr Gly Glu Cys Trp Ala Phe Ala Ala His Gln Asn Gly Gln Ser
57 35 40 45
58 Val Val Gln Asn Gly Met Tyr Lys Gly Phe Thr Leu Ser Glu Leu Trp
59 50 55 60
60 Glu His His Arg His Leu Phe Gly Gln Leu Glu Gly Asp Arg Phe Pro
61 65 70 75 80

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62 Leu Leu Thr Lys Ile Leu Asp Ala Asp Gln Asp Leu Ser Val Gln Val
63      85      90      95
64 His Pro Asn Asp Glu Tyr Ala Asn Ile His Glu Asn Gly Glu Leu Gly
65      100     105     110
66 Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Gln Lys Asp Ala Glu Ile
67      115     120     125
68 Ile Tyr Gly His Asn Ala Thr Thr Lys Glu Glu Leu Thr Thr Met Ile
69      130     135     140
70 Glu Arg Gly Glu Trp Asp Glu Leu Leu Arg Arg Val Lys Val Lys Pro
71      145     150     155     160
72 Gly Asp Phe Phe Tyr Val Pro Ser Gly Thr Val His Ala Ile Gly Lys
73      165     170     175
74 Gly Ile Leu Ala Leu Glu Thr Gln Gln Asn Ser Asp Thr Thr Tyr Arg
75      180     185     190
76 Leu Tyr Asp Tyr Asp Arg Lys Asp Ala Glu Gly Lys Leu Arg Glu Leu
77      195     200     205
78 His Leu Lys Lys Ser Ile Glu Val Ile Glu Val Pro Ser Ile Pro Glu
79      210     215     220
80 Arg His Thr Val His His Glu Gln Ile Glu Asp Leu Leu Thr Thr Thr
81      225     230     235     240
82 Leu Ile Glu Cys Ala Tyr Phe Ser Val Gly Lys Trp Asn Leu Ser Gly
83      245     250     255
84 Ser Ala Ser Leu Lys Gln Gln Lys Pro Phe Leu Leu Ile Ser Val Ile
85      260     265     270
86 Glu Gly Glu Gly Arg Met Ile Ser Gly Glu Tyr Val Tyr Pro Phe Lys
87      275     280     285
88 Lys Gly Asp His Met Leu Leu Pro Tyr Gly Leu Gly Glu Phe Lys Leu
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93 <210> SEQ ID NO: 3
94 <211> LENGTH: 220
95 <212> TYPE: PRT
96 <213> ORGANISM: Bacillus subtilis
98 <400> SEQUENCE: 3
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101 Gln Lys Gly Ala Val Thr Pro Val Lys Asn Gln Gly Ser Cys Gly Ser
102      20      25      30
103 Cys Trp Ala Phe Ser Ala Val Val Thr Ile Glu Gly Ile Ile Lys Ile
104      35      40      45
105 Arg Thr Gly Asn Leu Asn Glu Tyr Ser Glu Gln Glu Leu Leu Asp Cys
106      50      55      60
107 Asp Arg Arg Ser Tyr Gly Cys Asn Gly Gly Tyr Pro Trp Ser Ala Leu
108      65      70      75      80
109 Gln Leu Val Ala Gln Tyr Gly Ile His Tyr Arg Asn Thr Tyr Pro Tyr
110      85      90      95
111 Glu Gly Val Gln Arg Tyr Cys Arg Ser Arg Glu Lys Gly Pro Tyr Ala
112      100     105     110

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113 Ala Lys Thr Asp Gly Val Arg Gln Val Gln Pro Tyr Asn Glu Gly Ala
114      115      120      125
115 Leu Leu Tyr Ser Ile Ala Asn Gln Pro Val Ser Val Val Leu Glu Ala
116      130      135      140
117 Ala Gly Lys Asp Phe Gln Leu Tyr Arg Gly Gly Ile Phe Val Gly Pro
118      145      150      155      160
119 Cys Gly Asn Lys Val Asp His Ala Val Ala Val Gly Tyr Gly Pro
120      165      170      175
121 Asn Tyr Ile Leu Ile Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Asn
122      180      185      190
123 Gly Tyr Ile Arg Ile Lys Arg Gly Thr Gly Asn Ser Tyr Gly Val Cys
124      195      200      205
125 Gly Leu Tyr Thr Ser Ser Phe Tyr Pro Val Lys Asn
126      210      215      220
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129 <211> LENGTH: 948
130 <212> TYPE: DNA
131 <213> ORGANISM: Bacillus subtilis
133 <400> SEQUENCE: 4
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135 gctttacgag atagatttgg atacagtatt ccttcagaat caacggggga atgctggggc      120
136 atttccgctc atccaaaagg accgagcact gttgcaaatg gcccgataa aggaagaca      180
137 ttgatcgagc tttgggaaga gcaccgtgaa gtattcgggc gcgtagaggg ggatcggtt      240
138 ccgcttctga caaagctgct ggaatgtgaa gaagatacgt caaltaaagt tcacctgat      300
139 gattactatg ccggagaaaa cgaagaggga gaactcggca agacggaatg ctggtacatt      360
140 atcgactgta aggaaaacyc agaaatcatt tacgggcata cggcccgctc aaaaaaccgaa      420
141 cttgtcacia tgatcaacag cggtgactgg gagggcctgc tgcgaagaa caaaattaaa      480
142 ccgggtgatt totattatgt gccgagcggg acgtgcacg cattgtgcaa gggggccctt      540
143 gttttagaga ctacgcaaaa ttcagatgcc acataccggg tgtacgatta tgaccgtctt      600
144 gatagcaacy gaagtcggag agagcttcat ttggccaaag cggccaatgc cggcacgggt      660
145 ccccatgtgg acgggtatat agatgaatcg acagaatcaa gaaaaggaa aaccattaaa      720
146 acatttgtcc aaggggaata ttttcgggt tataaatggg acatcaatgg cgaagctgaa      780
147 atggtctcagg atgaatcctt totgatttgc agcgtgatag aagggaacgg tttgtcagg      840
148 tatgaggaca aaacatgtcc gctcaaaaaa ggtgatcact ttattttgcc ggctcaaatg      900
149 cccgatttta cgataaaaag aacttgtacc cttatcgtgt ctcatatt      948
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152 <211> LENGTH: 316
153 <212> TYPE: PRT
154 <213> ORGANISM: Bacillus subtilis
156 <400> SEQUENCE: 5
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159 Trp Gly Gly Thr Ala Leu Arg Asp Arg Phe Gly Tyr Ser Ile Pro Ser
160      20      25      30
161 Glu Ser Thr Gly Glu Cys Trp Ala Ile Ser Ala His Pro Lys Gly Pro
162      35      40      45
163 Ser Thr Val Ala Asn Gly Pro Tyr Lys Gly Lys Thr Leu Ile Glu Leu
164      50      55      60
165 Trp Glu Glu His Arg Glu Val Phe Gly Gly Val Glu Gly Asp Arg Phe

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166	65	70	75	80
167	Pro Leu Leu Thr Lys Leu Leu Asp Val Lys Glu Asp Thr Ser Ile Lys			
168	85	90	95	
169	Val His Pro Asp Asp Tyr Tyr Ala Gly Glu Asn Glu Glu Gly Glu Leu			
170	100	105	110	
171	Gly Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Lys Glu Asn Ala Glu			
172	115	120	125	
173	Ile Ile Tyr Gly His Thr Ala Arg Ser Lys Thr Glu Leu Val Thr Met			
174	130	135	140	
175	Ile Asn Ser Gly Asp Trp Glu Gly Leu Leu Arg Arg Ile Lys Ile Lys			
176	145	150	155	160
177	Pro Gly Asp Phe Tyr Tyr Val Pro Ser Gly Thr Leu His Ala Leu Cys			
178	165	170	175	
179	Lys Gly Ala Leu Val Leu Glu Thr Gln Gln Asn Ser Asp Ala Thr Tyr			
180	180	185	190	
181	Arg Val Tyr Asp Tyr Asp Arg Leu Asp Ser Asn Gly Ser Pro Arg Glu			
182	195	200	205	
183	Leu His Phe Ala Lys Ala Val Asn Ala Ala Thr Val Pro His Val Asp			
184	210	215	220	
185	Gly Tyr Ile Asp Glu Ser Thr Glu Ser Arg Lys Gly Ile Thr Ile Lys			
186	225	230	235	240
187	Thr Phe Val Gln Gly Glu Tyr Phe Ser Val Tyr Lys Trp Asp Ile Asn			
188	245	250	255	
189	Gly Glu Ala Glu Met Ala Gln Asp Glu Ser Phe Leu Ile Cys Ser Val			
190	260	265	270	
191	Ile Glu Gly Ser Gly Leu Leu Lys Tyr Glu Asp Lys Thr Cys Pro Leu			
192	275	280	285	
193	Lys Lys Gly Asp His Phe Ile Leu Pro Ala Gln Met Pro Asp Phe Thr			
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207	caggtgagtg	ctgggcccgtt	120	
208	tctgcacatg	cccatggctc	gtcgtctgtg	aaaaatggcc
209	cyctggcagg	aaagacactt	180	
210	gatcaagtat	ggaagatca	tccagagata	ttcgggtttc
211	cggatggtaa	ggtgtttccg	240	
212	ctgctggtaa	agctgctgga	cgccaatatg	gatctctccg
213	tgcaagtcca	tcctgatgat	300	
214	gattatgcaa	aactgcacga	aaatggcgac	cttggtaaaa
215	cggagtgcgtg	gtatatcatt	360	
216	gattgcaaa	atgacgcga	actaat	tttg
217	ggacatcatg	caagcaca	aa	ggaagagttc
218	420			
219	aaacaacgaa	tagaaagcgg	tgattggaac	gggctgctga
220	ggcgaatcaa	aatcaagcca	480	
221	ggagatttct	tttatgtgcc	aagcgggtaca	ctccatgctt
222	tatgtaagg	aacccttgtc	540	
223	cttgaaatcc	agcaaaactc	tgatacaaca	tatcgcgtat
224	acgattatga	ccgctgta	600	
225	gaccagggcc	aaaaaagaac	tcttcatata	gaaaaagcca
226	tggaagtc	aacgataccg	660	
227	catatcgata	aagtycat	accggaagta	aaagaagt
228	gtaacgctga	gatcattgtt	720	
229	tatgtgcaat	cagattat	ctcagtgtac	aaatggaaga
230	ttagcgccg	agctgctttt	780	

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217 ccttcataatc aaacctatatt gctggggagtg gttctgagcgc gatcaggacg aatcataaat      840
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219 gaatttacaa tagaaggaac atgtgaattc atgatatttc atcct      945
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223 <212> TYPE: PRT
224 <213> ORGANISM: Bacillus subtilis
226 <400> SEQUENCE: 7
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231 Lys Thr Gly Glu Cys Trp Ala Val Ser Ala His Ala His Gly Ser Ser
232 35 40 45
233 Ser Val Lys Asn Gly Pro Leu Ala Gly Lys Thr Leu Asp Gln Val Trp
234 50 55 60
235 Lys Asp His Pro Glu Ile Phe Gly Phe Pro Asp Gly Lys Val Phe Pro
236 65 70 75 80
237 Leu Leu Val Lys Leu Leu Asp Ala Asn Met Asp Leu Ser Val Gln Val
238 85 90 95
239 His Pro Asp Asp Asp Tyr Ala Lys Leu His Glu Asn Gly Asp Leu Gly
240 100 105 110
241 Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Lys Asp Asp Ala Glu Leu
242 115 120 125
243 Ile Leu Gly His His Ala Ser Thr Lys Glu Glu Phe Lys Gln Arg Ile
244 130 135 140
245 Glu Ser Gly Asp Trp Asn Gly Leu Leu Arg Arg Ile Lys Ile Lys Pro
246 145 150 155 160
247 Gly Asp Phe Phe Tyr Val Pro Ser Gly Thr Leu His Ala Leu Cys Lys
248 165 170 175
249 Gly Thr Leu Val Leu Glu Ile Gln Gln Asn Ser Asp Thr Thr Tyr Arg
250 180 185 190
251 Val Tyr Asp Tyr Asp Arg Cys Asn Asp Gln Gly Gln Lys Arg Thr Leu
252 195 200 205
253 His Ile Glu Lys Ala Met Glu Val Ile Thr Ile Pro His Ile Asp Lys
254 210 215 220
255 Val His Thr Pro Glu Val Lys Glu Val Gly Asn Ala Glu Ile Ile Val
256 225 230 235 240
257 Tyr Val Gln Ser Asp Tyr Phe Ser Val Tyr Lys Trp Lys Ile Ser Gly
258 245 250 255
259 Arg Ala Ala Phe Pro Ser Tyr Gln Thr Tyr Leu Leu Gly Ser Val Leu
260 260 265 270
261 Ser Gly Ser Gly Arg Ile Ile Asn Asn Gly Ile Gln Tyr Glu Cys Asn
262 275 280 285
263 Ala Gly Ser His Phe Ile Leu Pro Ala His Phe Gly Glu Phe Thr Ile
264 290 295 300
265 Glu Gly Thr Cys Glu Phe Met Ile Ser His Pro
266 305 310 315

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VERIFICATION SUMMARY

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